

STIC-Biotech/ChemLib

196715

From: Bausch, Sarae
Sent: Wednesday, July 26, 2006 5:37 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 10/663497

Please do a standard nucleic acid sequence search encoding the amino acid sequence of SEQ ID No. 25, residues 158-163, for 10/663497. Please print out the first 50 hits.

Thank you.

Sarae Bausch, Ph.D.
USPTO Art Unit 1634
REM 2 A 70
Mailbox: REM 2 C 70
(571) 272-2912

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 1, 2006, 10:35:50 ; Search time 2272 Seconds

(without alignments)
221.511 Million cell updates/sec

Title: US-10-663-497A-25_COPY_158_163

Perfect score: 31

Sequence: 1 MTTVP 6

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh
-Q-/abs/ABSWEB_spool/US10663497/runat_01082006_083600_1288/app_query.fasta_1
-DB=EST -QFMT=fastap -SUPPLX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.0.cdi -LIST=150
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs06h
-USER=US10663497 @CN1.1 4769 @runat_01082006_083600_1288 -NCPU=6 -ICPU=3
-NO_MAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPEXT=0.5 -FGAPOPEXT=7
-FGAPOPEXT=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database :

EST: *
1: gb_est1: *
2: gb_est3: *
3: gb_est4: *
4: gb_est5: *
5: gb_est6: *
6: gb_hic: *
7: gb_est2: *
8: gb_est7: *
9: gb_est8: *
10: gb_est9: *
11: gb_ges1: *
12: gb_ges2: *
13: gb_ges3: *
14: gb_ges4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	180	1	AJ463628
2	31	100.0	217	7	BB112240
3	31	100.0	223	13	CL221902
4	31	100.0	230	7	BB063656

5	31	100.0	240	2	BF900869
6	31	100.0	249	1	AV282051
7	31	100.0	250	1	AV142411
8	31	100.0	251	1	AV330138
9	31	100.0	258	13	CZ259261
c	10	31	268	8	CV831343
	11	31	269	7	BB420250
	12	31	275	7	BB720743
c	13	31	281	1	AI650253
c	14	31	281	5	CK880041
	15	31	282	7	BB455432
	16	31	284	7	BB194369
	17	31	284	7	BB407564
	18	31	284	8	CK363247
	19	31	287	7	BB386771
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	21	31	291	7	BB192244
	22	31	291	7	BB405411
c	23	31	292	7	BB432442
	24	31	297	7	BB339341
	25	31	299	7	BB375154
	26	31	301	7	BB123949
	27	31	302	7	BB137719
	28	31	304	7	BB463421
	29	31	306	7	BB122366
	30	31	308	10	DY218704
	31	31	316	7	BB257508
	32	31	316	7	BB367725
c	33	31	317	10	W36164
	34	31	318	7	AW604092
	35	31	326	11	BB610392
	36	31	328	4	BY123236
	37	31	331	4	BY103137
	38	31	331	7	BB131656
	39	31	331	7	BB207693
	40	31	331	7	BB249936
	41	31	331	13	CL366355
	42	31	333	4	BY304673
	43	31	334	12	CG512001
	44	31	342	4	CL13316
	45	31	344	12	CG086613
c	46	31	346	8	CV428815
	47	31	350	7	AW308438
c	48	31	356	12	CE293776
	49	31	360	9	BE624513
	50	31	360	9	D69147
c	51	31	363	2	BG629299
	52	31	363	7	BE688274
	53	31	366	12	CG495711
	54	31	374	12	CG611802
c	55	31	378	7	AV766938
	56	31	381	8	CN470928
	57	31	382	12	CG500417
c	58	31	383	1	AI504289
	59	31	383	12	CG508897
	60	31	384	1	AV202038
c	61	31	388	3	BQ499068
	62	31	388	12	CG577010
c	63	31	389	1	AA752646
	64	31	389	12	CG503960
	65	31	392	1	AI117812
	66	31	395	1	AA250694
	67	31	395	10	W53543
	68	31	395	12	CG631195
	69	31	397	1	AA031074
	70	31	397	4	BY105532
	71	31	401	12	CG503954
	72	31	401	14	CNS06GDT
	73	31	402	12	CG545882
	74	31	402	12	CG512943
	75	31	402	12	CG642888
c	76	31	403	12	CG508603
	77	31	403	12	CG576780

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80	31	100.0	404	12	CG511362	OST63684
81	31	100.0	404	12	CG610121	OST292460
82	31	100.0	405	12	CG055853	SALK_0977
83	31	100.0	405	12	CG508250	OST58762
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85	31	100.0	406	11	BH014919	TDCBSA6TH
86	31	100.0	408	4	BY093847	BY093847
87	31	100.0	410	1	AA268982	va99d06.r
88	31	100.0	411	4	BY288280	BY288280
89	31	100.0	414	4	BX515944	BX515944
90	31	100.0	419	7	AW479331	24715 MAR
91	31	100.0	421	3	BO598023	QGG18B18
92	31	100.0	422	7	BE555107	u449b08.y
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94	31	100.0	423	11	AQ640114	927P1-2D1
95	31	100.0	424	7	BE600010	P11 78.D0
96	31	100.0	424	7	AA524192	ng36g09.s
97	31	100.0	425	1	AW287335	LGI_269.F
98	31	100.0	432	7	AG255606	Lotus_cor
99	31	100.0	439	14	BF195890	7087a02.x
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103	31	100.0	453	10	DV421484	NADYS70TR
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108	31	100.0	466	7	BE448145	ut80b03.y
109	31	100.0	466	7	BE597646	P11 72.D0
110	31	100.0	468	1	AA194371	zq05c03.s
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113	31	100.0	470	7	BE448495	ut90f01.y
114	31	100.0	470	7	BE599215	P11 86.G0
115	31	100.0	477	7	BE650827	UI-M-BH3-
116	31	100.0	477	7	BE653213	UI-M-ANO-
117	31	100.0	481	7	AW489629	UI-M-BH3-
118	31	100.0	481	7	AW493902	UI-M-BH3-
119	31	100.0	482	2	B1173984	OSTF009H5
120	31	100.0	491	1	AA690651	vu53e10.r
121	31	100.0	497	4	BX511885	BX511885
122	31	100.0	500	5	CD599903	CK121A3A0
123	31	100.0	503	1	AA386922	vc23d12.r
124	31	100.0	505	7	AW624748	EST122693
125	31	100.0	507	4	CA249653	SCRUFLL11
126	31	100.0	511	7	AW944928	EST336978
127	31	100.0	512	7	AW490025	UI-M-BH3-
128	31	100.0	514	10	DV552243	122000b11
129	31	100.0	517	7	BE595457	P11_55.G0
130	31	100.0	519	2	B1927198	EST547087
131	31	100.0	519	7	BB867484	BB867484
132	31	100.0	519	7	BE599938	P11 77.B1
133	31	100.0	519	10	DT177202	JGI_ANNO4
134	31	100.0	520	1	AU249853	AU249853
135	31	100.0	520	11	AZ132104	OSUNBB005
136	31	100.0	521	7	BF470230	UI-M-BH3-
137	31	100.0	522	7	BE596226	P11 51.B0
138	31	100.0	524	4	BX525148	BX525148
139	31	100.0	524	7	AW494870	UI-M-BH3-
140	31	100.0	526	4	CB438008	685913.MA
141	31	100.0	527	2	B1211968	IP1_62.G0
142	31	100.0	533	2	BF923102	QV4-NT025
143	31	100.0	534	9	DB351716	DB351716
144	31	100.0	534	12	CG680080	ZWMBB0032
145	31	100.0	537	12	BZ635050	OCB105TM
146	31	100.0	538	11	BH015137	TGGBV42TH
147	31	100.0	540	4	BX557881	BX557881
148	31	100.0	544	8	CN185253	UCRC05_0
149	31	100.0	545	1	AJ407475	AJ407475
150	31	100.0	545	11	AZ254990	RPCI-23-1

ALIGNMENTS

RESULT 1

AJ463628

LOCUS

DEFINITION

AJ463628

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 180)

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Location/Qualifiers

1..180

/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"

/cultivar="Saana"

/sub_species="vulgare"

/db_xref="taxon:112509"

/clone="S0000200077F10F1"

/dev_stage="Embryo"

/clone_lib="S00002"

/note="1 day after pollination"

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-663-497A-25_COPY_158_163 (1-6) x AJ463628 (1-180)

Qy

1 MetThrThrThrValPro 6

Db

33 ATGACGACAACTGTACCA 50

RESULT 2

BH112240

LOCUS

DEFINITION

BH112240

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 217)

AUTHORS

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
Hirose, T., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayata, N.,
Hirose, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadoya, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 1, 2006, 10:23:46 ; Search time 418 Seconds
(without alignments)
150.120 Million cell updates/sec

Title: US-10-663-497A-25_COPY_158_163

Perfect score: 31

Sequence: 1 MTTVP 6

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-DB=N_Geneseq -QFMT=fastcap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=bloum62 -TRANS=human40.cdi -LIST=150
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02h
-USR=US10663497 @CGM_1_1761 @runat_01082006_083556_1248 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_8.*

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2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005as.*
15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	18	14	ADY98104
2	31	100.0	25	9	ACH65851
3	31	100.0	39	12	ADL64531

4	31	100.0	153	13	ADS01729	AdS01729 Staphyloc
5	31	100.0	420	6	ABN92824	Abn92824 Staphyloc
6	31	100.0	420	13	ADS02980	AdS02980 Staphyloc
c 7	31	100.0	430	6	ABN87768	Abn87768 Human pro
8	31	100.0	453	10	ADB51509	AdB51509 Primay r
9	31	100.0	496	14	ADY98093	AdY98093 Human TIM
10	31	100.0	499	14	ADY98092	AdY98092 Human TIM
c 11	31	100.0	509	4	AAH88202	AaH88202 CNS diseo
12	31	100.0	554	13	ACN46715	Acn46715 Cotton pr
c 13	31	100.0	648	13	ADR59534	AdR59534 Cotton cd
c 14	31	100.0	784	10	ADC30255	AdC30255 Human nov
15	31	100.0	804	14	AEC32074	AeC32074 Human CG5
16	31	100.0	906	4	AAH53216	AaH53216 S. epider
c 17	31	100.0	930	8	ABZ52453	AbZ52453 Aspergill
c 18	31	100.0	1059	6	ABZ14283	AbZ14283 Arabidops
c 19	31	100.0	1059	8	ADA68644	Ada68644 Arabidops
20	31	100.0	1095	10	ABZ68336	AbZ68336 Nucleotid
21	31	100.0	1095	14	ADY98080	AdY98080 Human TIM
22	31	100.0	1095	14	AED60524	AeD60524 Human TIM
23	31	100.0	1098	10	ABZ68334	AbZ68334 Nucleotid
24	31	100.0	1098	14	ADY98076	AdY98076 Human TIM
25	31	100.0	1098	14	AED60520	AeD60520 Human TIM
26	31	100.0	1113	11	ACL33708	AcL33708 Rice abio
c 27	31	100.0	1274	14	ACL72110	AcL72110 M. xanthu
c 28	31	100.0	1319	2	AAH06841	AaH06841 Arabidops
c 29	31	100.0	1336	3	AAH47532	AaH47532 Arabidops
c 30	31	100.0	1339	3	AAH34681	AaH34681 Arabidops
31	31	100.0	1448	4	AAH29729	AaH29729 S cerevis
32	31	100.0	1857	12	ADO35434	AdO35434 Novel mou
c 33	31	100.0	1884	13	ADS60328	AdS60328 Bacterial
c 34	31	100.0	2000	11	ACL34911	AcL34911 Rice stre
35	31	100.0	3112	4	AAH16200	AaH16200 Human CDN
36	31	100.0	3150	13	ADQ87365	AdQ87365 Human tum
c 37	31	100.0	3259	4	AAH54766	AaH54766 S. epider
38	31	100.0	3349	4	AAH54143	AaH54143 S. epider
39	31	100.0	3713	4	AAH54416	AaH54416 S. epider
40	31	100.0	11382	14	ACL64441	AcL64441 M. xanthu
41	31	100.0	27204	11	ACN44866	Acn44866 Human gen
42	31	100.0	37500	12	ADH48029	AdH48029 Clone PS3
43	31	100.0	67212	3	AAA08954	AaA08954 WFS1 vari
44	31	100.0	92112	13	ACN44736	AcN44736 Mouse gen
c 45	31	100.0	107320	11	ACN44736	AcN44736 Mouse gen
c 46	31	100.0	118935	14	ADZ13136	AdZ13136 Murine ca
47	31	100.0	123219	4	AAH88703	AaH88703 Human DNA
c 48	31	100.0	138627	12	ADQ97183	AdQ97183 Human can
c 49	31	100.0	151830	12	ADH51151	AdH51151 Protein p
c 50	31	100.0	151830	12	ADH78027	AdH78027 Human PPP
c 51	31	100.0	151830	14	AEA48114	Aea48114 Human PPP
52	31	100.0	193789	14	AED89415	AeD89415 Human bre
53	30	96.8	21	2	AAH34897	AaH34897 PCR prime
54	30	96.8	318	1	AAH50343	AaH50343 DNA encod
55	30	96.8	321	14	AED43896	AeD43896 Human epi
c 56	30	96.8	351	2	AAH51681	AaH51681 Human sec
c 57	30	96.8	444	11	ACL28553	AcL28553 Rice abio
58	30	96.8	455	8	ABZ52892	AbZ52892 Aspergill
c 59	30	96.8	491	6	ABN24660	Abn24660 Human ORF
60	30	96.8	642	13	ADS48827	AdS48827 Bacterial
61	30	96.8	651	12	ADJ42877	AdJ42877 Plant tra
62	30	96.8	793	5	ABA18007	AbA18007 Human ner
63	30	96.8	1029	8	ADC29993	AdC29993 Plant ful
64	30	96.8	1038	3	ACA38856	AcA38856 Prokaryot
65	30	96.8	1308	10	ABX07812	AbX07812 S. pneumo
66	30	96.8	1308	12	ADM92007	AdM92007 S. pneumo
67	30	96.8	1311	13	ADK45553	AdK45553 Streptoco
68	30	96.8	1323	13	ADR93963	AdR93963 Novel S.
69	30	96.8	1323	14	AEA57833	Aea57833 Streptoco
c 70	30	96.8	1407	8	ACA30774	AcA30774 Prokaryot
c 71	30	96.8	1436	2	AAV52429	AaV52429 Streptoco
c 72	30	96.8	1607	5	AAF83842	Aaf83842 C. pneumo
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c 74	30	96.8	1684	12	ADM47742	AdM47742 Polynucle
c 75	30	96.8	1971	10	ADF42467	AdF42467 Human PP8
c 76	30	96.8	2065	3	AAC44909	Aac44909 Arabidops

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 1, 2006, 10:31:51 ; Search time 3418 Seconds
(without alignments)
168.381 Million cell updates/sec

Title: US-10-663-497a-25_COPY_158_163

Perfect score: 31

Sequence: 1 MTTVP 6

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abse/ABSSWEB_spool/US10663497/runat_01082006_083558_1259/app_query.fasta.1
-DB=GenEmbl -OPMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -
-UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi -LIST=150
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb_env.*
2: gb_pat.*
3: gb_ph.*
4: gb_pl.*
5: gb_pr.*
6: gb_ro.*
7: gb_sts.*
8: gb_sy.*
9: gb_un.*
10: gb_v1.*
11: gb_ov.*
12: gb_hcg.*
13: gb_in.*
14: gb_om.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	31 100.0	411 7	BV236381	S234P6518
2	31 100.0	420 15	AB101460	Streptococ
3	31 100.0	441 4	AY14867	Saccharom

4	31	100.0	447	15	AY186969	Trichloro
5	31	100.0	509	2	AX194572	Sequence
6	31	100.0	520	4	AY144866	Saccharom
7	31	100.0	591	7	BV283028	S232P6162
8	31	100.0	667	5	AY448733	Cercocebu
9	31	100.0	718	7	BV663407	S217P6008
10	31	100.0	863	7	BV032503	S212P6885
11	31	100.0	906	2	AR484494	Sequence
12	31	100.0	906	2	AX143103	Sequence
13	31	100.0	948	8	DQ331823	Synthetic
14	31	100.0	950	7	BV479132	td112c10.
15	31	100.0	951	4	AY144967	Saccharom
16	31	100.0	954	6	BC099515	Mus muscu
17	31	100.0	1026	7	CNS061PY	T3 end of
18	31	100.0	1041	7	CNS06FT3	AL396433
19	31	100.0	1059	2	AX507393	Sequence
20	31	100.0	1059	2	AX651611	Sequence
21	31	100.0	1104	2	AR550575	Sequence
22	31	100.0	1243	6	BC058428	Mus muscu
23	31	100.0	1274	2	AR627172	Sequence
24	31	100.0	1319	2	AR575922	Sequence
25	31	100.0	1319	4	AF061638	Arabidops
26	31	100.0	1448	2	AX072920	Sequence
27	31	100.0	2194	4	SCU46559	Saccharomyc
28	31	100.0	3020	4	SCYNR034W	Z71649 S.cerevisia
29	31	100.0	3112	2	BD158192	Primer fo
30	31	100.0	3112	2	AX880097	Sequence
31	31	100.0	3112	5	AK023070	Homo sapi
32	31	100.0	3259	2	AR486044	Sequence
33	31	100.0	3259	2	AX145408	Sequence
34	31	100.0	3259	15	AF270090	Staphyloc
35	31	100.0	3349	2	AR485421	Sequence
36	31	100.0	3349	2	AX144785	Sequence
37	31	100.0	3349	15	AF269465	Staphyloc
38	31	100.0	3703	15	DQ028634	Mycobacte
39	31	100.0	3713	2	AR485694	Sequence
40	31	100.0	3713	2	AX145058	Sequence
41	31	100.0	3713	15	AF269740	Staphyloc
42	31	100.0	3840	4	YSCPAMIBEN	Yeast para-
43	31	100.0	4259	4	SCU43608	Saccharomyc
44	31	100.0	9389	15	STE250581	Sequence
45	31	100.0	11382	2	AR619509	Streptococ
46	31	100.0	11425	15	AE009708	Brucella
47	31	100.0	13380	5	HSV11740	H.sapiens w
48	31	100.0	13759	15	AE005041	Halobacte
49	31	100.0	26276	13	U88177	Caenorhabd1
50	31	100.0	37500	2	CQ767413	Sequence
51	31	100.0	37500	2	CQ774651	Sequence
52	31	100.0	43158	12	CR933778	Danio rer
53	31	100.0	49295	11	BX571669	Zebrafish
54	31	100.0	53951	5	AC092866	Homo sapi
55	31	100.0	56963	12	CR974590_3	Continuation (4 of
56	31	100.0	61744	12	AL713961	Danio rer
57	31	100.0	61817	11	AL749527	Zebrafish
58	31	100.0	62246	12	AC180220	Strongylo
59	31	100.0	63649	1	AY576273	Bacterioph
60	31	100.0	69614	12	AC083925	Homo sapi
61	31	100.0	71506	5	AC092452	Homo sapi
62	31	100.0	73431	12	AP000575	Homo sapi
63	31	100.0	84208	12	AP008109	Lotus cor
64	31	100.0	84388	5	AL589984	Human DNA
65	31	100.0	85975	5	AC110011	Homo sapi
66	31	100.0	87230	12	AP007492	Lotus cor
67	31	100.0	87967	4	AC005223	Arabidops
68	31	100.0	88917	11	AL929169	Zebrafish
69	31	100.0	92112	2	CQ893967	Sequence
70	31	100.0	95356	5	AL139112	Human DNA
71	31	100.0	96217	5	AL645729	Human DNA
72	31	100.0	96579	11	CR848001	Zebrafish
73	31	100.0	97512	5	AL139351	Human DNA
74	31	100.0	98461	4	ATT6H20	Arabidops
75	31	100.0	103979	12	AC167040	Bos tauru
76	31	100.0	104423	12	AP008156	Lotus cor

77	31	100.0	105075	12	CT573793	CT573793 Danio rerio
78	31	100.0	106886	5	AP001462	AP001462 Homo sapi
79	31	100.0	107415	5	AL513365	AL513365 Human DNA
80	31	100.0	107480	5	AC073118	AC073118 Homo sapi
81	31	100.0	107965	5	AC093678	AC093678 Homo sapi
82	31	100.0	109290	12	HS838L14	Y12335 Homo sapien
83	31	100.0	110000	4	AP008212_050	Continuation (51 o
84	31	100.0	110000	4	AP008212_207	Continuation (208
85	31	100.0	110000	4	AP008213_149	Continuation (150
86	31	100.0	110000	4	AP008216_217	Continuation (218
87	31	100.0	110000	4	CR380959_10	Continuation (11 o
88	31	100.0	110000	4	CR382123_07	Continuation (8 of
89	31	100.0	110000	4	CR382132_38	Continuation (39 o
90	31	100.0	110000	4	CR382135_11	Continuation (12 o
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92	31	100.0	110000	4	AE016959_217	Continuation (218 o
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94	31	100.0	110000	4	AE017345_09	Continuation (10 o
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96	31	100.0	110000	4	AP007157_08	Continuation (9 of
97	31	100.0	110000	4	AP008207_216	Continuation (217
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99	31	100.0	110000	12	AC140527_2	Continuation (3 of
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103	31	100.0	110000	12	TANN11_05	Continuation (10 o
104	31	100.0	110000	12	TANN3_06	Continuation (7 of
105	31	100.0	110000	12	TANN3_07	Continuation (8 of
106	31	100.0	110000	15	CP000089_17	Continuation (18 o
107	31	100.0	110000	15	CP000094_08	Continuation (9 of
108	31	100.0	110000	15	CP000097_15	Continuation (16 o
109	31	100.0	110000	15	CP000110_05	Continuation (6 of
110	31	100.0	110000	15	CP000112_15	Continuation (16 o
111	31	100.0	110000	15	CP000143_00	CP000143 Rhodobact
112	31	100.0	110000	15	CP000155_12	Continuation (13 o
113	31	100.0	110000	15	CR543861_13	Continuation (14 o
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117	31	100.0	110000	15	AE015928_22	Continuation (23 o
118	31	100.0	110000	15	AE016825_44	Continuation (45 o
119	31	100.0	110000	15	AE016825_45	Continuation (46 o
120	31	100.0	110000	15	AE017224_06	Continuation (7 of
121	31	100.0	110000	15	AE017285_06	Continuation (7 of
122	31	100.0	110000	15	AM040265_06	Continuation (7 of
123	31	100.0	110000	15	AP006618_49	Continuation (50 o
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126	31	100.0	110000	15	BA000002_15	Continuation (16 o
127	31	100.0	110000	15	BA000012_58	Continuation (59 o
128	31	100.0	110000	15	BA000014_64	Continuation (65 o
129	31	100.0	110000	15	BA000030_68	Continuation (69 o
130	31	100.0	110000	15	CP000029_13	Continuation (14 o
131	31	100.0	110000	15	CP000029_22	Continuation (23 o
132	31	100.0	110334	12	AC170219	AC170219 Bos tauru
133	31	100.0	113053	12	AC108087	AC108087

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 4, 2006, 19:20:46 ; Search time 102 Seconds

(without alignments)
139.750 Million cell updates/sec

Title: US-10-663-497A-25_COPY_158_163

Perfect score: 31

Sequence: 1 MTTTVP 6

Scoring table:

BLOSUM62	
Xgapop 10.0, Xgapext 0.5	
Ygapop 10.0, Ygapext 0.5	
Fgapop 6.0, Fgapext 7.0	
Delop 6.0, Delext 7.0	

Searched: 2193277 seqs, 791917567 residues

Total number of hits satisfying chosen parameters: 4386554

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=xlh
-O=/abss/ABSSWEB_spool/US10663497/runat_01082006_083608_1450/app_query.fasta 1
-NA=Published Applications NA New -QFMT=faatap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LODCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cgi -LIST=150 -DOCALLS=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=50 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abss804
-USER=US10663497@CGN_1_91 @runat_01082006_083608_1450 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WAEN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7

Database :

Published Applications NA.New.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	25	7	US-11-348-413-436439 Sequence 436439,
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7	31	100.0	25	7	US-11-348-413-1077807 Sequence 1077807,
8	31	100.0	25	7	US-11-348-413-1143851 Sequence 1143851,

9	31	100.0	25	7	US-11-348-413-1143852 Sequence 1143852,
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14	31	100.0	25	7	US-11-348-413-1143857 Sequence 1143857,
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c 19	31	100.0	25	7	US-11-348-413-1189180 Sequence 1189180,
c 20	31	100.0	25	7	US-11-348-413-1189181 Sequence 1189181,
c 21	31	100.0	25	7	US-11-348-413-1189182 Sequence 1189182,
c 22	31	100.0	25	7	US-11-348-413-1189183 Sequence 1189183,
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24	31	100.0	122	7	US-11-348-413-14913 Sequence 14913, A
c 25	31	100.0	122	7	US-11-348-413-16206 Sequence 16206, A
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ALIGNMENTS

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; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 436439
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 13150; WAN01UP87; Start 595; Stop 619;
; OTHER INFORMATION: 00000000011111
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Score: 31.00 Matches: 6
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0
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; Sequence 436440, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 436440
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
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GenCore version 5.1.9
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Run on: August 1, 2006, 11:00:04 ; Search time 1451 Seconds
        (without alignments)
        76.216 Million cell updates/sec

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Perfect score: 31
Sequence: 1 MTTTVP 6

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                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop 6.0 , Delext 7.0

Searched: 1892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 150 summaries

Command line parameters: -DB=frame+ p2n.model -DEV=xlp
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-MINMATCH=0.1 -LOOPLC=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES
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Result Query
No. Score Match Length DB ID Description
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c	74	30	96.8	318	8	US-10-437-963-46048	Sequence 46048, A

75	30	96.8	349	8	US-10-424-599-19004	Sequence 19004, A																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
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